

#2



PCT

## RAW SEQUENCE LISTING

DATE: 10/06/2004

PATENT APPLICATION: US/10/509,622

TIME: 16:11:42

Input Set : A:\Q83855 Sequence Listing.txt

Output Set: N:\CRF4\10062004\J509622.raw

3 <110> APPLICANT: Yamanouchi Pharmaceutical Co. Ltd  
 4 Masakatsu KAWAKAMI  
 6 <120> TITLE OF INVENTION: NOVEL OXIDASE  
 8 <130> FILE REFERENCE: Q83855  
 C--> 10 <140> CURRENT APPLICATION NUMBER: US/10/509,622  
 C--> 10 <141> CURRENT FILING DATE: 2004-09-29  
 10 <150> PRIOR APPLICATION NUMBER: PCT/JP03/07148  
 11 <151> PRIOR FILING DATE: 2003-06-05  
 13 <150> PRIOR APPLICATION NUMBER: JP 2002-165612  
 14 <151> PRIOR FILING DATE: 2002-06-06  
 16 <150> PRIOR APPLICATION NUMBER: JP 2002-060749  
 17 <151> PRIOR FILING DATE: 2003-03-07  
 19 <160> NUMBER OF SEQ ID NOS: 13  
 21 <170> SOFTWARE: PatentIn version 3.1  
 23 <210> SEQ ID NO: 1  
 24 <211> LENGTH: 1548  
 25 <212> TYPE: DNA  
 26 <213> ORGANISM: Homo sapiens  
 28 <220> FEATURE:  
 29 <221> NAME/KEY: CDS  
 30 <222> LOCATION: (1)..(1548)  
 32 <400> SEQUENCE: 1

33 atg gga aac tgg gtg gtt aac cac tgg ttt tca gtt ttg ttt ctg gtt	48
34 Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val	
35 1 5 10 15	
37 gtt tgg tta ggg ctg aat gtt ttc ctg ttt gtg gat gcc ttc ctg aaa	96
38 Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys	
39 20 25 30	
41 tat gag aag gcc gac aaa tac tac tac aca aga aaa atc ctt ggg tca	144
42 Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser	
43 35 40 45	
45 aca ttg gcc tgt gcc cga gcg tct gct ctc tgc ttg aat ttt aac agc	192
46 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser	
47 50 55 60	
49 acg ctg atc ctg ctt cct gtg tgt cgc aat ctg ctg tcc ttc ctg agg	240
50 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg	
51 65 70 75 80	
53 ggc acc tgc tca ttt tgc agc cgc aca ctg aga aag caa ttg gat cac	288
54 Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His	
55 85 90 95	
57 aac ctc acc ttc cac aag ctg gtg gcc tat atg atc tgc cta cat aca	336
58 Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr	
59 100 105 110	



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61	gct att cac atc att gca cac ctg ttt aac ttt gac tgc tat agc aga	384
62	Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg	
63	115 120 125	
65	agc cga cag gcc aca gat ggc tcc ctt gcc tcc att ctc tcc agc cta	432
66	Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu	
67	130 135 140	
69	tct cat gat gag aaa aag ggg ggt tct tgg cta aat ccc atc cag tcc	480
70	Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser	
71	145 150 155 160	
73	cga aac acg aca gtg gag tat gtg aca ttc acc agc gtt gct ggt ctc	528
74	Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Val Ala Gly Leu	
75	165 170 175	
77	act gga gtg atc atg aca ata gcc ttg att ctc atg gta act tca gct	576
78	Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala	
79	180 185 190	
81	act gag ttc atc cgg agg agt tat ttt gaa gtc ttc tgg tat act cac	624
82	Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His	
83	195 200 205	
85	cac ctt ttt atc ttc tat atc ctt ggc tta ggg att cac ggc att ggt	672
86	His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly	
87	210 215 220	
89	gga att gtc cgg ggt caa aca gag gag agc atg aat gag agt cat cct	720
90	Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro	
91	225 230 235 240	
93	cgc aag tgt gca gag tct ttt gag atg tgg gat gat cgt gac tcc cac	768
94	Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His	
95	245 250 255	
97	tgt agg cgc cct aag ttt gaa ggg cat ccc cct gag tct tgg aag tgg	816
98	Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp	
99	260 265 270	
101	atc ctt gca ccg gtc att ctt tat atc tgt gaa agg atc ctc cgg ttt	864
102	Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe	
103	275 280 285	
105	tac cgc tcc cag cag aag gtt gtg att acc aag gtt gtt atg cac cca	912
106	Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro	
107	290 295 300	
109	tcc aaa gtt ttg gaa ttg cag atg aac aag cgt ggc ttc agc atg gaa	960
110	Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu	
111	305 310 315 320	
113	gtg ggg cag tat atc ttt gtt aat tgc ccc tca atc tct ctc ctg gaa	1008
114	Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu	
115	325 330 335	
117	tgg cat cct ttt act ttg acc tct gct cca gag gaa gat ttc ttc tcc	1056
118	Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser	
119	340 345 350	
121	att cat atc cga gca gca ggg gac tgg aca gaa aat ctc ata agg gct	1104
122	Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala	
123	355 360 365	
125	ttc gaa caa caa tat tca cca att ccc agg att gaa gtg gat ggt ccc	1152

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126 Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
127      370                      375                      380
129 ttt ggc aca gcc agt gag gat gtt ttc cag tat gaa gtg gct gtg ctg      1200
130 Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
131 385                      390                      395                      400
133 gtt gga gca gga att ggg gtc acc ccc ttt gct tct atc ttg aaa tcc      1248
134 Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
135      405                      410                      415
137 atc tgg tac aaa ttc cag tgt gca gac cac aac ctc aaa aca aaa aag      1296
138 Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
139      420                      425                      430
141 gtt ggt cat gca gca tta aac ttt gac aag gcc act gac atc gtg aca      1344
142 Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
143      435                      440                      445
145 ggt ctg aaa cag aaa acc tcc ttt ggg aga cca atg tgg gac aat gag      1392
146 Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
147      450                      455                      460
149 ttt tct aca ata gct acc tcc cac ccc aag tct gta gtg gga gtt ttc      1440
150 Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
151 465                      470                      475                      480
153 tta tgt ggc cct cgg act ttg gca aag agc ctg cgc aaa tgc tgt cac      1488
154 Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
155      485                      490                      495
157 cga tat tcc agt ctg gat cct aga aag gtt caa ttc tac ttc aac aaa      1536
158 Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys
159      500                      505                      510
161 gaa aat ttt tga      1548
162 Glu Asn Phe
163      515
166 <210> SEQ ID NO: 2
167 <211> LENGTH: 515
168 <212> TYPE: PRT
169 <213> ORGANISM: Homo sapiens
171 <400> SEQUENCE: 2
173 Met Gly Asn Trp Val Val Asn His Trp Phe Ser Val Leu Phe Leu Val
174 1      5      10      15
177 Val Trp Leu Gly Leu Asn Val Phe Leu Phe Val Asp Ala Phe Leu Lys
178      20      25      30
181 Tyr Glu Lys Ala Asp Lys Tyr Tyr Tyr Thr Arg Lys Ile Leu Gly Ser
182      35      40      45
185 Thr Leu Ala Cys Ala Arg Ala Ser Ala Leu Cys Leu Asn Phe Asn Ser
186      50      55      60
189 Thr Leu Ile Leu Leu Pro Val Cys Arg Asn Leu Leu Ser Phe Leu Arg
190 65      70      75      80
193 Gly Thr Cys Ser Phe Cys Ser Arg Thr Leu Arg Lys Gln Leu Asp His
194      85      90      95
197 Asn Leu Thr Phe His Lys Leu Val Ala Tyr Met Ile Cys Leu His Thr
198      100     105     110
201 Ala Ile His Ile Ile Ala His Leu Phe Asn Phe Asp Cys Tyr Ser Arg

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202          115          120          125
205 Ser Arg Gln Ala Thr Asp Gly Ser Leu Ala Ser Ile Leu Ser Ser Leu
206          130          135          140
209 Ser His Asp Glu Lys Lys Gly Gly Ser Trp Leu Asn Pro Ile Gln Ser
210 145          150          155          160
213 Arg Asn Thr Thr Val Glu Tyr Val Thr Phe Thr Ser Val Ala Gly Leu
214          165          170          175
217 Thr Gly Val Ile Met Thr Ile Ala Leu Ile Leu Met Val Thr Ser Ala
218          180          185          190
221 Thr Glu Phe Ile Arg Arg Ser Tyr Phe Glu Val Phe Trp Tyr Thr His
222          195          200          205
225 His Leu Phe Ile Phe Tyr Ile Leu Gly Leu Gly Ile His Gly Ile Gly
226          210          215          220
229 Gly Ile Val Arg Gly Gln Thr Glu Glu Ser Met Asn Glu Ser His Pro
230 225          230          235          240
233 Arg Lys Cys Ala Glu Ser Phe Glu Met Trp Asp Asp Arg Asp Ser His
234          245          250          255
237 Cys Arg Arg Pro Lys Phe Glu Gly His Pro Pro Glu Ser Trp Lys Trp
238          260          265          270
241 Ile Leu Ala Pro Val Ile Leu Tyr Ile Cys Glu Arg Ile Leu Arg Phe
242          275          280          285
245 Tyr Arg Ser Gln Gln Lys Val Val Ile Thr Lys Val Val Met His Pro
246          290          295          300
249 Ser Lys Val Leu Glu Leu Gln Met Asn Lys Arg Gly Phe Ser Met Glu
250 305          310          315          320
253 Val Gly Gln Tyr Ile Phe Val Asn Cys Pro Ser Ile Ser Leu Leu Glu
254          325          330          335
257 Trp His Pro Phe Thr Leu Thr Ser Ala Pro Glu Glu Asp Phe Phe Ser
258          340          345          350
261 Ile His Ile Arg Ala Ala Gly Asp Trp Thr Glu Asn Leu Ile Arg Ala
262          355          360          365
265 Phe Glu Gln Gln Tyr Ser Pro Ile Pro Arg Ile Glu Val Asp Gly Pro
266          370          375          380
269 Phe Gly Thr Ala Ser Glu Asp Val Phe Gln Tyr Glu Val Ala Val Leu
270 385          390          395          400
273 Val Gly Ala Gly Ile Gly Val Thr Pro Phe Ala Ser Ile Leu Lys Ser
274          405          410          415
277 Ile Trp Tyr Lys Phe Gln Cys Ala Asp His Asn Leu Lys Thr Lys Lys
278          420          425          430
281 Val Gly His Ala Ala Leu Asn Phe Asp Lys Ala Thr Asp Ile Val Thr
282          435          440          445
285 Gly Leu Lys Gln Lys Thr Ser Phe Gly Arg Pro Met Trp Asp Asn Glu
286          450          455          460
289 Phe Ser Thr Ile Ala Thr Ser His Pro Lys Ser Val Val Gly Val Phe
290 465          470          475          480
293 Leu Cys Gly Pro Arg Thr Leu Ala Lys Ser Leu Arg Lys Cys Cys His
294          485          490          495
297 Arg Tyr Ser Ser Leu Asp Pro Arg Lys Val Gln Phe Tyr Phe Asn Lys
298          500          505          510

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301 Glu Asn Phe
302      515
305 <210> SEQ ID NO: 3
306 <211> LENGTH: 28
307 <212> TYPE: DNA
308 <213> ORGANISM: Homo sapiens
310 <400> SEQUENCE: 3
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314 <210> SEQ ID NO: 4
315 <211> LENGTH: 30
316 <212> TYPE: DNA
317 <213> ORGANISM: Homo sapiens
319 <400> SEQUENCE: 4
320 aaaatgcaga ttaccgtcct tattccttaa      30
323 <210> SEQ ID NO: 5
324 <211> LENGTH: 27
325 <212> TYPE: DNA
326 <213> ORGANISM: Homo sapiens
328 <400> SEQUENCE: 5
329 aaaacaaaaa aggttggtca tgcagca      27
332 <210> SEQ ID NO: 6
333 <211> LENGTH: 21
334 <212> TYPE: DNA
335 <213> ORGANISM: Homo sapiens
337 <400> SEQUENCE: 6
338 tcaaaaattt tctttgttga a      21
341 <210> SEQ ID NO: 7
342 <211> LENGTH: 20
343 <212> TYPE: DNA
344 <213> ORGANISM: Homo sapiens
346 <400> SEQUENCE: 7
347 accacagtcc atgccatcac      20
350 <210> SEQ ID NO: 8
351 <211> LENGTH: 20
352 <212> TYPE: DNA
353 <213> ORGANISM: Homo sapiens
355 <400> SEQUENCE: 8
356 tccaccaccc tgttgctgta      20
359 <210> SEQ ID NO: 9
360 <211> LENGTH: 19
361 <212> TYPE: DNA
362 <213> ORGANISM: Homo sapiens
364 <400> SEQUENCE: 9
365 attgcctctg aattcaaca      19
368 <210> SEQ ID NO: 10
369 <211> LENGTH: 18
370 <212> TYPE: DNA
371 <213> ORGANISM: Homo sapiens
373 <400> SEQUENCE: 10

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VERIFICATION SUMMARY

DATE: 10/06/2004

PATENT APPLICATION: US/10/509,622

TIME: 16:11:43

Input Set : A:\Q83855 Sequence Listing.txt

Output Set: N:\CRF4\10062004\J509622.raw

L:10 M:270 C: Current Application Number differs, Replaced Current Application No

L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date